IFWO

RAW SEQUENCE LISTING   DATE: 08/02/2004
PATENT APPLICATION: US/10/829,250   TIME: 14:37:42

Input Set : **N:\Crf3\RULE60\10829250.raw**
Output Set: **N:\CRF4\08022004\J829250.raw**

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 1 <110> APPLICANT: HATTORI, NORIAKI
 2       MURAKAMI, SEIJI
 3 <120> TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP
USING THE
 4       SAME
 5 <130> FILE REFERENCE: 193582US-3524-7126-0 PCT
 6 <140> CURRENT APPLICATION NUMBER: US/10/829,250
 7 <141> CURRENT FILING DATE: 2004-04-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/581,241
 9 <151> PRIOR FILING DATE: 2000-06-26
10 <150> PRIOR APPLICATION NUMBER: JP97/361022
11 <151> PRIOR FILING DATE: 1997-12-26
12 <160> NUMBER OF SEQ ID NOS: 8
13 <170> SOFTWARE: PatentIn version 3.2
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 23
17 <212> TYPE: DNA
18 <213> ORGANISM: ARTIFICIAL SEQUENCE
19 <220> FEATURE:
20 <223> OTHER INFORMATION: SYNTHETIC DNA
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24 <210> SEQ ID NO: 2
25 <211> LENGTH: 23
26 <212> TYPE: DNA
27 <213> ORGANISM: ARTIFICIAL SEQUENCE
28 <220> FEATURE:
29 <223> OTHER INFORMATION: SYNTHETIC DNA
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34 <211> LENGTH: 1644
35 <212> TYPE: DNA
36 <213> ORGANISM: Luciola lateralis
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1644)
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43       1               5                   10                  15
44       ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat      96
45       Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
46                       20                  25                  30
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47    atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt    144
48    Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
49            35                  40                  45
50    acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt    192
51    Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
52            50                  55                  60
53    cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att    240
54    Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
55    65                  70                  75                  80
56    gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc    288
57    Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
58                        85                  90                  95
59    ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act    336
60    Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
61                        100                 105                 110
62    cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta    384
63    Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
64                115                 120                 125
65    ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg    432
66    Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
67            130                 135                 140
68    gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat    480
69    Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
70    145                 150                 155                 160
71    aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa    528
72    Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
73                        165                 170                 175
74    ggt ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa    576
75    Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
76                        180                 185                 190
77    caa gtt gct ctt ata atg aac tct tcg ggt tca acc ggt ttg cca aaa    624
78    Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
79                195                 200                 205
80    ggt gtg caa ctt act cat gaa aat ttg gtc act aga ttt tct cac gct    672
81    Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala
82            210                 215                 220
83    aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta    720
84    Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
85    225                 230                 235                 240
86    act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc    768
87    Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
88                        245                 250                 255
89    tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa    816
90    Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
91                        260                 265                 270
92    gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att    864
93    Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
94                275                 280                 285
95    ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat    912
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 96      Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
 97          290                 295                 300
 98      aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct      960
 99      Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
100      305                 310                 315                 320
101      tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg      1008
102      Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
103                          325                 330                 335
104      ggt gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att      1056
105      Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
106                  340                 345                 350
107      atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg      1104
108      Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
109              355                 360                 365
110      cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg      1152
111      Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
112          370                 375                 380
113      ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg      1200
114      Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
115      385                 390                 395                 400
116      aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa      1248
117      Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
118                          405                 410                 415
119      gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa      1296
120      Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
121                  420                 425                 430
122      cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga      1344
123      His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
124              435                 440                 445
125      tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca      1392
126      Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
127          450                 455                 460
128      aat att ttt gat gcc ggc gtt gct ggc gtt cca gat cct ata gct ggt      1440
129      Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
130      465                 470                 475                 480
131      gag ctt ccg gga gct gtt gtt gta ctt aag aaa gga aaa tct atg act      1488
132      Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
133                          485                 490                 495
134      gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa      1536
135      Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
136                  500                 505                 510
137      cgt ttg cgt ggt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc      1584
138      Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
139              515                 520                 525
140      act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca      1632
141      Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
142          530                 535                 540
143      gtt gct aag atg                                                      1644
144      Val Ala Lys Met
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Output Set: **N:\CRF4\08022004\J829250.raw**

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147 <210> SEQ ID NO: 4
148 <211> LENGTH: 548
149 <212> TYPE: PRT
150 <213> ORGANISM: Luciola lateralis
151 <400> SEQUENCE: 4
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154     Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
155                 20                  25                  30
156     Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
157             35                  40                  45
158     Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
159         50                  55                  60
160     Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
161     65                  70                  75                  80
162     Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
163                 85                  90                  95
164     Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
165                 100                 105                 110
166     Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
167             115                 120                 125
168     Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
169             130                 135                 140
170     Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
171     145                 150                 155                 160
172     Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
173                 165                 170                 175
174     Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
175                 180                 185                 190
176     Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
177             195                 200                 205
178     Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala
179         210                 215                 220
180     Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
181     225                 230                 235                 240
182     Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
183                 245                 250                 255
184     Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
185                 260                 265                 270
186     Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
187             275                 280                 285
188     Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
189         290                 295                 300
190     Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
191     305                 310                 315                 320
192     Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
193                 325                 330                 335
194     Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
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195                   340              345              350
196      Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
197             355              360              365
198      Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
199         370              375              380
200      Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
201      385              390              395              400
202      Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
203                  405              410              415
204      Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
205             420              425              430
206      His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
207             435              440              445
208      Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
209          450              455              460
210      Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
211      465              470              475              480
212      Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
213                  485              490              495
214      Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
215             500              505              510
216      Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
217             515              520              525
218      Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
219         530              535              540
220      Val Ala Lys Met
221         545
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 1644
225 <212> TYPE: DNA
226 <213> ORGANISM: Luciola lateralis
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (1)..(1644)
230 <400> SEQUENCE: 5
231      atg gaa aac atg gag aac gat gaa aat att gtg tat ggt cct gaa cca      48
232      Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
233      1               5                   10                  15
234      ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat      96
235      Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
236                  20                  25                  30
237      atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt     144
238      Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
239             35                  40                  45
240      acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt     192
241      Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
242         50                  55                  60
243      cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att     240
244      Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/02/2004
PATENT APPLICATION: **US/10/829,250**   TIME: 14:37:43

Input Set : **N:\Crf3\RULE60\10829250.raw**
Output Set: **N:\CRF4\08022004\J829250.raw**

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VERIFICATION SUMMARY   DATE: 08/02/2004
PATENT APPLICATION: **US/10/829,250**   TIME: 14:37:43

Input Set : **N:\Crf3\RULE60\10829250.raw**
Output Set: **N:\CRF4\08022004\J829250.raw**